

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 23:02:39 ; Search time 356.058 Seconds
(without alignments)
384.253 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 conacgtncknccrcytcrcg 23

Scoring table: IDENTITY_NUC

Searched: Gapop 10_0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 311075104

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 500 summaries

Database : Published Applications NA:*

1: /cggn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cggn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cggn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:*

4: /cggn2_6/ptodata/1/pubpna/US05_PUBCOMB.seq:*

5: /cggn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

6: /cggn2_6/ptodata/1/pubpna/PCTIS_PUBCOMB.seq:*

7: /cggn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cggn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cggn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

10: /cggn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cggn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cggn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cggn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*

14: /cggn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*

15: /cggn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cggn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*

17: /cggn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cggn2_6/ptodata/1/pubpna/US10_F_PUBCOMB.seq:*

19: /cggn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

20: /cggn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

21: /cggn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

22: /cggn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match Length	DB ID	Description
1	17.4	75.7	23	10 US-09-989-643-108 Sequence 108, App
2	17.4	75.7	23	18 US-10-753-169-108 Sequence 108, App
3	17.4	75.7	24	17 US-10-391-249-35 Sequence 35, Appl
4	17.4	75.7	98	9 US-09-815-242-607 Sequence 607, App
5	17.4	75.7	98	17 US-10-282-122A-626 Sequence 626, App
6	17.4	75.7	108	17 US-10-282-122A-3089 Sequence 3089, App
7	17.4	75.7	108	17 US-10-282-122A-3372 Sequence 3372, App
8	17.4	75.7	108	17 US-10-282-122A-3105 Sequence 3105, App
9	17.4	75.7	122	17 US-10-282-122A-11867 Sequence 11867, App
10	17.4	75.7	186	17 US-10-282-122A-11867 Sequence 11867, App
11	17.4	75.7	298	9 US-09-815-242-608 Sequence 608, App

Sequence 633, App
Sequence 2764, App
Sequence 2694, App
Sequence 5304, App
Sequence 2431, App
Sequence 2253, App
Sequence 8376, App
Sequence 1966, App
Sequence 2476, App
Sequence 12826, App
Sequence 37180, App
Sequence 149, App
Sequence 21, App
Sequence 149, App
Sequence 148, App
Sequence 148, App
Sequence 20, App
Sequence 152, App
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GenCore version 5.1.6									
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OM nucleic - nucleic search, using sw model									
Run on:	March 16, 2005, 01:07:34 ; Search time 87.1346 Seconds	(without alignment)	431.911 Million cell updates/sec						
Title:	US-10-089-177-697								
Perfect score:	23								
Sequence:	1 cncacngtncckccrcytcrg 23								
Scoring table:	IDENTITY_NUC	Gappop 10.0 , Gapext 1.0							
Searched:	1202784 seqs, 818138359 residues								
Minimum DB seq length:	0								
Maximum DB seq length:	2000000000								
Post-processing:	Minimum Match 0%								
	Maximum Match 100%								
	Listing first 500 summaries								
Database :	Issued Patents NA:*								
	1: /cggn2_6/pctodata/1/ina/5A_COMB.seq:*								
	2: /cggn2_6/pctodata/1/ina/5B_COMB.seq:*								
	3: /cggn2_6/pctodata/1/ina/6A_COMB.seq:*								
	4: /cggn2_6/pctodata/1/ina/6B_COMB.seq:*								
	5: /cggn2_6/pctodata/1/ina/PCTUS_COMB.seq:*								
	6: /cggn2_6/pctodata/1/ina/backfiles1.seq:*								
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score	Query	Match Length	DB ID	Description				
1	17.4	75.7	189	4 US-09-107-532A-31602	Sequence 3602, AP				
2	17.4	75.7	297	4 US-09-252-991A-4695	Sequence 4695, AP				
3	17.4	75.7	330	4 US-09-107-532A-1603	Sequence 1603, AP				
4	17.4	75.7	498	4 US-09-902-540-7475	Sequence 7475, AP				
5	17.4	75.7	609	4 US-09-107-433-2243	Sequence 2243, AP				
6	17.4	75.7	785	3 US-09-154-083-29	Sequence 29, Appl				
7	17.4	75.7	1122	4 US-09-134-000C-1261	Sequence 1261, AP				
8	17.4	75.7	1131	4 US-09-107-532A-979	Sequence 979, AP				
9	17.4	75.7	1155	4 US-09-328-352-1547	Sequence 1547, AP				
10	17.4	75.7	1185	2 US-08-743-637B-185	Sequence 185, APP				
11	17.4	75.7	1185	3 US-09-218-197-1	Sequence 1, Appl				
12	17.4	75.7	1185	4 US-09-492-709A-86	Sequence 86, Appl				
13	17.4	75.7	1191	4 US-09-107-532A-1379	Sequence 1379, AP				
14	17.4	75.7	1191	4 US-09-902-540-8380	Sequence 8380, AP				
15	17.4	75.7	1197	4 US-09-583-110-747	Sequence 747, APP				
16	17.4	75.7	1224	4 US-09-252-991A-4775	Sequence 4775, AP				
17	17.4	75.7	1230	4 US-09-252-991A-4773	Sequence 4773, AP				
18	17.4	75.7	1230	4 US-09-252-991A-4767	Sequence 4767, AP				
19	17.4	75.7	1245	3 US-09-134-001C-2540	Sequence 2540, AP				
20	17.4	75.7	1284	4 US-09-489-039A-3648	Sequence 3648, AP				
21	17.4	75.7	1260	4 US-09-039A-3750	Sequence 3750, AP				
22	17.4	75.7	1356	4 US-09-252-991A-4740	Sequence 4740, AP				
23	17.4	75.7	2995	3 US-08-61-527-260	Sequence 260, APP				
24	17.4	75.7	3719	1 US-08-920-812-10	Sequence 10, APP				
25	17.4	75.7	3719	1 US-08-920-827-10	Sequence 10, APP				
26	17.4	75.7	3719	1 US-08-921-177-10	Sequence 10, APP				
27	17.4	75.7	3719	1 US-08-362-577C-10	Sequence 10, APP				

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OM nucleic - nucleic search, using sw model
Run on: March 15, 2005, 22:27:13 ; Search time 2312.38 Seconds
(without alignments)
378.604 Million cell updates/sec

Title: US-10-089-177-697
Perfect score: 23
Sequence: 1 cccacngtncnccrccttcgtcgg 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues
Total number of hits satisfying chosen parameters: 368479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : EST,*
1: gb_eat1:/*
2: gb_eat2:/*
3: gb_hcc:/*
4: gb_eat3:/*
5: gb_eat4:/*
6: gb_eat5:/*
7: gb_eat6:/*
8: gb_gb81:/*
9: gb_gb82:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
C 1	17.4	75.7	190	6	CD163898	CD163898_M11-0084T
C 2	17.4	75.7	259	6	CD180022	CD180022_MS1-0021T
C 3	17.4	75.7	365	7	CN028509	CN028509_UNC-pbliv
C 4	17.4	75.7	372	7	CN026743	CN026743_UNC-paciv
C 5	17.4	75.7	422	1	AU007630	AU007630_ATTO07630
C 6	17.4	75.7	465	1	AU010926	AU010926_AU010926
C 7	17.4	75.7	518	5	BQ811177	BQ811177_BQ811177
C 8	17.4	75.7	527	4	BQ821805	BQ821805_10300950
C 9	17.4	75.7	539	5	BQ812860	BQ812860_103003240
C 10	17.4	75.7	566	1	BQ815804	BQ815804_10300533A0
C 11	17.4	75.7	570	8	CC107141	CC107141_NDL-13F13
C 12	17.4	75.7	579	5	BQ809961	BQ809961_1030014D0
C 13	17.4	75.7	626	5	BQ809962	BQ809962_1030014D0
C 14	17.4	75.7	637	6	CB3302236	CB3302236_1030021B0
C 15	17.4	75.7	712	7	COT755154	COT755154_Mdrt3048
C 16	17.4	75.7	718	7	CO255523	CO255523_WS00825.B
C 17	17.4	75.7	777	9	CL698612	CL698612_PR1017C.B
C 18	17.4	75.7	1122	8	BZ549591	BZ549591_pacsl1-60-
C 19	16.4	71.3	424	6	CB3302190	CB3302190_TGST72f9
C 20	16.4	71.3	471	6	CB3302236	CB3302236_TGST72f9
C 21	16.4	71.3	505	2	BP252980	BP252980_EST443475
C 22	16.4	71.3	531	7	CO151838	CO151838_EST822891
C 23	16.4	71.3	538	6	CA15033	CA15033_SCJTR203
C 24	16.4	71.3	545	7	CF939964	CF939964_NCESTqabs
C 97	15.8	68.7	272	6	AU248181	AU248181_AU248181
C 98	15.8	68.7	272	6	CA282200	CA282200_SCAGSD204

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Run on: March 15, 2005, 15:46:58 ; Search time 296.346 Seconds
 (without alignments)
 45.443 Million cell updates/sec

OM nucleic - nucleic search, using sw model

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 cccnacgttcknccrccttcgg 23

Scoring table: IDENTITY_NUC

Searched: Gapext 1.0

Total number of hits satisfying chosen parameters: 38780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : N_Geneseq_16pec04,*

1: geneseqn1980s:*

2: geneseqn1990s:*

3: geneseqn2000s:*

4: geneseqn2001as:*

5: geneseqn2001bs:*

6: geneseqn2002as:*

7: geneseqn2002bs:*

8: geneseqn2003as:*

9: geneseqn2003bs:*

10: geneseqn2003cs:*

11: geneseqn2003ds:*

12: geneseqn2004as:*

13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	17.4	75.7	23 AAV37107	Aav37107 Oligonucleotide
2	17.4	75.7	23 AAK00706	Aah00706 Universal
3	17.4	75.7	24 AAC58471	Acf58471 M. hyorhi
4	17.4	75.7	98 AAS4693	Aas46930 Enterococcus
5	17.4	75.7	8 ACR12756	Aca12756 Prokaryot
6	17.4	75.7	108 ACR15502	Aca15502 Prokaryot
7	17.4	75.7	8 ACR15219	Aca15219 Prokaryot
8	17.4	75.7	108 ACR15070	Aca15070 Prokaryot
9	17.4	75.7	122 ACR13225	Aca13225 Prokaryot
10	17.4	75.7	6 ABM69463	Abm6946 Striptoo
11	17.4	75.7	8 ACR23997	Aca23997 Prokaryot
12	17.4	75.7	189 ACR17434	Aca17434 Prokaryot
13	17.4	75.7	297 11 ABD0691	Abd0691 Pseudomonas
14	17.4	75.7	298 4 AAS48031	Aas48031 Enterococcus
15	17.4	75.7	8 ACR12763	Aca12763 Prokaryot
16	17.4	75.7	305 4 AAS50187	Aas50187 Staphylococcus
17	17.4	75.7	8 ACT14824	Aca14824 Prokaryot
18	17.4	75.7	305 8 ACT14734	Aca14734 Prokaryot
19	17.4	75.7	10 ADC91976	Adc91976 E. faecium
20	17.4	75.7	341 10 ADC914561	Aca14561 Prokaryot

Result No.	Score	Query Match Length	DB ID	Description
21	17.4	75.7	383 8 ACA14383	Aca14383 Prokaryot
22	17.4	75.7	402 8 ACA20506	Aca20506 Prokaryot
23	17.4	75.7	402 10 ACA31596	Aca31596 Prokaryot
24	17.4	75.7	402 10 ABZ41635	Abz41635 N. gonorrhoeae
25	17.4	75.7	402 10 ABZ41135	Aca14605 Prokaryot
26	17.4	75.7	447 8 ACR24956	Aca24956 Prokaryot
27	17.4	75.7	448 8 ACA49510	Aca49510 Prokaryot
28	17.4	75.7	468 8 AAS89338	Aas89338 DNA encod
29	17.4	75.7	476 10 ABZ41132	Abz41132 N. gonorrhoeae
30	17.4	75.7	567 10 ABZ41633	Aca14605 Prokaryot
31	17.4	75.7	609 13 ADR93608	Adr93608 Novellus
32	17.4	75.7	693 6 ABX66003	Abx66003 Helicobacter
33	17.4	75.7	785 4 AAV37144	Aav37144 Chlamydia
34	17.4	75.7	888 4 AAH01746	Aah01746 Burkholderia
35	17.4	75.7	882 4 AAH01743	Aah01743 Bacteroides
36	17.4	75.7	882 4 AAV37160	Aav37160 DNA sequce
37	17.4	75.7	885 2 AAV37147	Aav37147 DNA sequce
38	17.4	75.7	891 2 AAV37163	Aav37163 Bacteriobacillus
39	17.4	75.7	888 2 AAV37151	Aav37151 DNA sequce
40	17.4	75.7	888 4 AAV37154	Aav37154 DNA sequce
41	17.4	75.7	891 2 AAV37152	Aav37152 DNA sequce
42	17.4	75.7	891 2 AAV37159	Aav37159 DNA sequce
43	17.4	75.7	891 2 AAV37152	Aav37152 DNA sequce
44	17.4	75.7	891 2 AAV37153	Aav37153 DNA sequce
45	17.4	75.7	891 2 AAV37161	Aav37161 DNA sequce
46	17.4	75.7	891 2 AAV37154	Aav37154 DNA sequce
47	17.4	75.7	891 2 AAV37152	Aav37152 DNA sequce
48	17.4	75.7	891 2 AAV37158	Aav37158 DNA sequce
49	17.4	75.7	891 2 AAV37159	Aav37159 DNA sequce
50	17.4	75.7	891 2 AAV37162	Aav37162 DNA sequce
51	17.4	75.7	891 4 AAH01750	Aah01750 Micrococcus
52	17.4	75.7	891 4 AAH01754	Aah01754 Rickettsia
53	17.4	75.7	891 4 AAH01752	Aah01752 Mycoplasma
54	17.4	75.7	891 4 AAH01755	Aah01755 Escherichia
55	17.4	75.7	891 4 AAH01753	Aah01753 Neisseria
56	17.4	75.7	891 4 AAH01751	Aah01751 Mycobacteria
57	17.4	75.7	891 4 AAH00619	Aah00619 Haemophilus
58	17.4	75.7	891 4 AAH01755	Aah01755 Salmonella
59	17.4	75.7	891 4 AAH01747	Aah01747 Fibrobacter
60	17.4	75.7	894 2 AAV37155	Aav37155 DNA sequce
61	17.4	75.7	894 2 AAV37150	Aav37150 DNA sequce
62	17.4	75.7	894 2 AAV37166	Aav37166 DNA sequce
63	17.4	75.7	894 4 AAH01745	Aah01745 Brevibacter
64	17.4	75.7	894 4 AAH01711	Aah01711 Streptococcus
65	17.4	75.7	894 4 AAH01748	Aah01748 Plasmabacter
66	17.4	75.7	894 4 AAS89341	Aas89341 DNA encod
67	17.4	75.7	894 5 AAS89387	Aas89387 DNA encod
68	17.4	75.7	895 5 AAS89354	Aas89354 DNA encod
69	17.4	75.7	895 5 AAS8927	Aas8927 DNA encod
70	17.4	75.7	897 2 AAV37165	Aav37165 DNA sequce
71	17.4	75.7	897 2 AAV37167	Aav37167 DNA sequce
72	17.4	75.7	897 2 AAV37146	Aav37146 DNA sequce
73	17.4	75.7	897 4 AAH01757	Aah01757 Stigmatelmatophora
74	17.4	75.7	897 4 AAH01741	Aah01741 Agrobacterium
75	17.4	75.7	897 4 AAH01758	Aah01758 Thiomonas
76	17.4	75.7	900 4 AAH02145	Aah02145 Pseudomonas
77	17.4	75.7	906 2 AAV37157	Aav37157 DNA sequce
78	17.4	75.7	906 4 AAH01749	Aah01749 Helicobacter
79	17.4	75.7	909 2 AAV37170	Aav37170 DNA sequce
80	17.4	75.7	909 2 AHR01761	Ahr01761 Molinella
81	17.4	75.7	918 8 ACA43477	Aca43477 Prokaryot
82	17.4	75.7	950 8 ACA5266	Aca5266 Prokaryot
83	17.4	75.7	968 2 AAV07942	Aav07942 Nucleotid
84	17.4	75.7	970 2 AAV08973	Aav08973 Nucleotid
85	17.4	75.7	1098 10 ABZ41217	Abz41217 N. gonorrhoeae
86	17.4	75.7	1098 10 ABZ41217	Abz41217 N. gonorrhoeae
87	17.4	75.7	1105 6 ABA96108	Abba96108 Schizosaccharomyces
88	17.4	75.7	1122 10 ADH83376	Adh83376 Enteroococcus
89	17.4	75.7	1131 10 ADC91352	Adc91352 E. faecium
90	17.4	75.7	1155 9 ADA3260	Ada3260 DNA encod
91	17.4	75.7	1170 2 AAQ20217	Aaq20217 Sequence
92	17.4	75.7	1182 4 ABT14914	Abt14914 Pathogen

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 22:08:52 ; Search time 874.442 Seconds
 (without alignments) 1274.492 Million cell updates/sec

Title: US-10-089-177-697

Perfect score: 23

Sequence: 1 ccnacngtncnccrcytcrg 23

Scoring table: IDENTITY_NUC

Searched: Gapext 1.0

Total number of hits satisfying chosen parameters: 39416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 500 summaries

Database : GenEmbl,*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_on:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ror:*

11: gb_sts:*

12: gb_sv:*

13: gb_uni:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	17.4	75.7	23	6	AX109964	AX109964 Sequence
2	17.4	75.7	23	6	BD023040	BD023040 Species-s
3	17.4	75.7	135	6	C0649882	C0649882 Sequence
4	17.4	75.7	189	6	AR348991	AR348991 Sequence
5	17.4	75.7	330	6	AR346992	AR346992 Sequence
6	17.4	75.7	1	SM75481	SM75481 Streptococcus	
7	17.4	75.7	693	6	AX788739	AX788739 Sequence
8	17.4	75.7	723	1	SPRSP10A	SPRSP10A Sequence
9	17.4	75.7	762	1	AF295388	AF295388 Sequence
10	17.4	75.7	882	6	AX110003	AX110003 Sequence
11	17.4	75.7	882	6	BD023081	BD023081 Species-s
12	17.4	75.7	1	AX11002	AX11002 Sequence	
13	17.4	75.7	885	6	BD023080	BD023080 Species-s
14	17.4	75.7	888	6	AX110006	AX110006 Sequence
15	17.4	75.7	888	6	AX110102	AX110102 Sequence
16	17.4	75.7	888	6	BD023084	BD023084 Species-s
17	17.4	75.7	891	6	AX109877	AX109877 Sequence
18	17.4	75.7	891	6	AX110935	AX110935 Sequence
19	17.4	75.7	891	6	AX110007	AX110007 Sequence
20	17.4	75.7	891	6	AX11010	AX11010 Sequence
21	17.4	75.7	891	6	AX11011	AX11011 Sequence
22	17.4	75.7	891	6	AX11012	AX11012 Sequence
23	17.4	75.7	891	6	AX11013	AX11013 Sequence
24	17.4	75.7	891	6	AX11014	AX11014 Sequence
25	17.4	75.7	891	6	AX11015	AX11015 Sequence
26	17.4	75.7	891	6	BD023086	BD023086 Species-s
27	17.4	75.7	891	6	BD023087	BD023087 Species-s
28	17.4	75.7	891	6	BD023089	BD023089 Species-s
29	17.4	75.7	891	6	BD023091	BD023091 Species-s
30	17.4	75.7	891	6	BD023092	BD023092 Species-s
31	17.4	75.7	891	6	BD023093	BD023093 Species-s
32	17.4	75.7	891	6	BD023094	BD023094 Species-s
33	17.4	75.7	891	6	BD023095	BD023095 Species-s
34	17.4	75.7	891	6	BD023096	BD023096 Species-s
35	17.4	75.7	894	6	AX11069	AX11069 Sequence
36	17.4	75.7	894	6	AX111005	AX111005 Sequence
37	17.4	75.7	894	6	AX111008	AX111008 Sequence
38	17.4	75.7	894	6	BD023083	BD023083 Species-s
39	17.4	75.7	894	6	BD023088	BD023088 Species-s
40	17.4	75.7	894	6	BD023100	BD023100 Species-s
41	17.4	75.7	897	6	AX111001	AX111001 Sequence
42	17.4	75.7	897	6	AX111017	AX111017 Sequence
43	17.4	75.7	897	6	AX111018	AX111018 Sequence
44	17.4	75.7	897	6	BD023079	BD023079 Species-s
45	17.4	75.7	897	6	BD023098	BD023098 Species-s
46	17.4	75.7	897	6	BD023103	BD023103 Species-s
47	17.4	75.7	900	6	AX111405	AX111405 Sequence
48	17.4	75.7	906	6	AX111009	AX111009 Sequence
49	17.4	75.7	906	6	AX111021	AX111021 Sequence
50	17.4	75.7	909	6	BD023103	BD023103 Species-s
51	17.4	75.7	909	6	BD023168	BD023168 Species-s
52	17.4	75.7	968	6	BD0161867	BD0161867 Antigenic
53	17.4	75.7	970	6	BD0611998	BD0611998 Antigenic
54	17.4	75.7	1043	2	PFMABPC1	AL993362 Plasmodium Sequence
55	17.4	75.7	1122	6	AR35426	AR354224 Species-s
56	17.4	75.7	1128	1	FSS8856	X768856 F...succinogae Sequence
57	17.4	75.7	1131	6	AR346368	AR346368 Sequence
58	17.4	75.7	1140	5	X768705	X768705 S...aurantica Sequence
59	17.4	75.7	1143	1	AF295387	AF295387 Pirellula Sequence
60	17.4	75.7	1149	1	CA6367UP	X76854 C...aurantiac Sequence
61	17.4	75.7	1155	6	ARS18997	AR318997 Sequence
62	17.4	75.7	1176	1	AY099292	AY099292 Bartonell Sequence
63	17.4	75.7	1176	1	AY099294	AY099294 Rhodobact Sequence
64	17.4	75.7	1176	1	CVTUF	X77033 Chlorobium Sequence
65	17.4	75.7	1182	6	AX583738	AX583738 Sequence
66	17.4	75.7	1182	6	AX60422	AX60422 Sequence
67	17.4	75.7	1182	6	BD269414	BD269414 Sequence
68	17.4	75.7	1182	6	AY099226	AY099226 Sequence
69	17.4	75.7	1182	6	BD269414	BD269414 Gene iden
70	17.4	75.7	1185	6	CQ817257	CQ817257 Sequence
71	17.4	75.7	1185	6	CQ817259	CQ817259 Sequence
72	17.4	75.7	1185	6	AR230091	AR230091 Sequence
73	17.4	75.7	1185	6	AR493528	AR493528 Sequence
74	17.4	75.7	1185	6	AX109965	AX109965 Sequence
75	17.4	75.7	1185	6	AX111364	AX111364 Sequence
76	17.4	75.7	1185	6	AX363591	AX363591 Sequence
77	17.4	75.7	1185	12	AY305395	AY305395 Synthetic
78	17.4	75.7	1185	12	AY305396	AY305396 Synthetic
79	17.4	75.7	1185	12	AY305397	AY305397 Synthetic
80	17.4	75.7	1188	1	AB035461	AB035461 Porphyrom
81	17.4	75.7	1188	1	AB035462	AB035462 Porphyrom
82	17.4	75.7	1188	1	AB035463	AB035463 Porphyrom
83	17.4	75.7	1188	1	AB035464	AB035464 Porphyrom
84	17.4	75.7	1188	1	AB035465	AB035465 Porphyrom
85	17.4	75.7	1188	1	AB035466	AB035466 Bacteroid
86	17.4	75.7	1188	1	TOTUF	X770316 T...cellulatus Sequence
87	17.4	75.7	1188	1	CLTUF	X77035 C...lyticia tu Sequence
88	17.4	75.7	1188	1	RFL1324	X76667 F...ferrugine Sequence
89	17.4	75.7	1191	1	RF137986	AB033986 Myxobocu Sequence
90	17.4	75.7	1191	1	TCHO55TF	X76571 T...cuprinus Sequence
91	17.4	75.7	1191	6	AR348768	AR348768 Sequence
92	17.4	75.7	1191	6	AX110130	AX110130 Sequence

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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 23:02:39 ; Search time 448.942 Seconds
(without alignments)

384.253 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aayatgattacnacngngcgcncaratgg 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5537552 seqs, 297463231 residues

Total number of hits satisfying chosen parameters: 311075104

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA:*

1:	/cgn2_6/ptodata/1/pubpna/us07_PUBCOMB.seq:*	c	12	23.2	80.0	184	9	US-09-815-242-2185	Sequence 2185, AP
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*	c	13	23.2	80.0	184	17	US-10-282-122A-4758	Sequence 4758, AP
3:	/cgn2_6/ptodata/1/pubpna/us06_NEW_PUB.seq:*	c	14	23.2	80.0	185	17	US-10-282-122A-1866	Sequence 1866, AP
4:	/cgn2_6/ptodata/1/pubpna/us06_PUBCOMB.seq:*	c	15	23.2	80.0	185	17	US-10-282-122A-2139	Sequence 2139, AP
5:	/cgn2_6/ptodata/1/pubpna/us07_NEW_PUB.seq:*	c	16	23.2	80.0	187	9	US-09-815-242-194	Sequence 194, AP
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*	c	17	23.2	80.0	187	9	US-09-815-242-198	Sequence 198, AP
7:	/cgn2_6/ptodata/1/pubpna/us08_NEW_PUB.seq:*	c	18	23.2	80.0	187	17	US-10-282-122A-1784	Sequence 184, APP
8:	/cgn2_6/ptodata/1/pubpna/us08_PUBCOMB.seq:*	c	19	23.2	80.0	187	17	US-10-282-122A-202	Sequence 202, APP
9:	/cgn2_6/ptodata/1/pubpna/us09_PUBCOMB.seq:*	c	20	23.2	80.0	193	17	US-10-282-122A-2553	Sequence 2553, APP
10:	/cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*	c	21	23.2	80.0	196	17	US-10-282-122A-3396	Sequence 3396, APP
11:	/cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*	c	22	23.2	80.0	202	9	US-09-815-242-176	Sequence 176, APP
12:	/cgn2_6/ptodata/1/pubpna/us09c_PUBCOMB.seq:*	c	23	23.2	80.0	202	17	US-10-282-122A-164	Sequence 177, APP
13:	/cgn2_6/ptodata/1/pubpna/us10_PUBCOMB.seq:*	c	24	23.2	80.0	222	17	US-10-282-122A-1777	Sequence 2570, APP
14:	/cgn2_6/ptodata/1/pubpna/us10_PUBCOMB.seq:*	c	25	23.2	80.0	222	17	US-10-282-122A-2570	Sequence 301, APP
15:	/cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*	c	26	23.2	80.0	236	9	US-09-815-242-301	Sequence 280, APP
16:	/cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*	c	27	23.2	80.0	236	17	US-10-282-122A-280	Sequence 242, APP
17:	/cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*	c	28	23.2	80.0	269	9	US-09-815-242-242	Sequence 229, APP
18:	/cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*	c	29	23.2	80.0	329	17	US-10-282-122A-229	Sequence 2708, APP
19:	/cgn2_6/ptodata/1/pubpna/us10c_PUBCOMB.seq:*	c	30	23.2	80.0	332	17	US-10-282-122A-2146	Sequence 2146, APP
20:	/cgn2_6/ptodata/1/pubpna/us11c_PUBCOMB.seq:*	c	31	23.2	80.0	341	17	US-10-282-122A-2394	Sequence 2394, APP
21:	/cgn2_6/ptodata/1/pubpna/us60c_PUBCOMB.seq:*	c	32	23.2	80.0	341	17	US-10-282-122A-2527	Sequence 2527, APP
22:	/cgn2_6/ptodata/1/pubpna/us60c_PUBCOMB.seq:*	c	33	23.2	80.0	343	17	US-10-282-122A-1952	Sequence 1933, APP
		c	34	23.2	80.0	369	17	US-10-282-122A-252	Sequence 2252, APP
		c	35	23.2	80.0	390	17	US-10-282-122A-2619	Sequence 2619, APP
		c	36	23.2	80.0	501	17	US-10-282-122A-2146	Sequence 2146, APP
		c	37	23.2	80.0	501	17	US-10-282-122A-19211	Sequence 19211, A
		c	38	23.2	80.0	501	17	US-10-449-857A-24	Sequence 24, APP
		c	39	23.2	80.0	572	17	US-10-282-122A-1933	Sequence 782, APP
		c	40	23.2	80.0	580	17	US-10-282-122A-747	Sequence 747, APP
		c	41	23.2	80.0	580	17	US-10-424-599-105909	Sequence 5496, APP
		c	42	23.2	80.0	566	17	US-10-425-115-1132	Sequence 87, APP
		c	43	23.2	80.0	572	17	US-10-425-115-1132	Sequence 16207, A
		c	44	23.2	80.0	705	17	US-10-449-857A-24	Sequence 12865, APP
		c	45	23.2	80.0	705	17	US-10-449-857A-24	Sequence 56213, A
		c	46	23.2	80.0	748	18	US-10-437-963-56273	Sequence 105509, APP
		c	47	23.2	80.0	617	18	US-10-021-323-5496	Sequence 11485, APP
		c	48	23.2	80.0	628	17	US-10-122A-21485	Sequence 2126, A
		c	49	23.2	80.0	656	17	US-09-939-980-87	Sequence 1132, APP
		c	50	23.2	80.0	705	17	US-10-282-122A-16207	Sequence 150, APP
		c	51	23.2	80.0	705	17	US-10-437-963-56273	Sequence 153, APP
		c	52	23.2	80.0	840	17	US-10-424-599-105909	Sequence 154, APP
		c	53	23.2	80.0	840	17	US-10-282-122A-2126	Sequence 157, APP
		c	54	23.2	80.0	884	18	US-10-425-115-1132	Sequence 159, APP
		c	55	23.2	80.0	888	18	US-09-989-643-150	Sequence 160, APP
		c	56	23.2	80.0	888	18	US-10-989-643-150	Sequence 161, APP
		c	57	23.2	80.0	891	18	US-09-989-643-153	Sequence 162, APP
		c	58	23.2	80.0	891	18	US-09-989-643-154	Sequence 163, APP
		c	59	23.2	80.0	891	18	US-09-989-643-157	Sequence 164, APP
		c	60	23.2	80.0	891	18	US-09-989-643-159	Sequence 165, APP
		c	61	23.2	80.0	891	18	US-09-989-643-159	Sequence 166, APP
		c	62	23.2	80.0	891	18	US-09-989-643-161	Sequence 167, APP
		c	63	23.2	80.0	891	18	US-09-989-643-162	Sequence 168, APP
		c	64	23.2	80.0	891	18	US-09-989-643-163	Sequence 169, APP
		c	65	23.2	80.0	891	18	US-09-989-643-164	Sequence 170, APP
		c	66	23.2	80.0	891	18	US-09-989-643-170	Sequence 171, APP
		c	67	23.2	80.0	891	18	US-09-753-169-153	Sequence 172, APP
		c	68	23.2	80.0	891	18	US-10-753-169-154	Sequence 173, APP
		c	69	23.2	80.0	891	18	US-10-753-169-157	Sequence 174, APP
		c	70	23.2	80.0	891	18	US-10-753-169-159	Sequence 175, APP
		c	71	23.2	80.0	891	18	US-10-753-169-160	Sequence 176, APP
		c	72	23.2	80.0	891	18	US-10-753-169-161	Sequence 177, APP
		c	73	23.2	80.0	891	18	US-10-753-169-162	Sequence 178, APP
		c	74	23.2	80.0	891	18	US-10-753-169-163	Sequence 179, APP
		c	75	23.2	80.0	891	18	US-10-753-169-164	Sequence 180, APP
		c	76	23.2	80.0	891	18	US-10-753-169-170	Sequence 181, APP
		c	77	23.2	80.0	894	18	US-09-989-643-151	Sequence 182, APP
		c	78	23.2	80.0	894	18	US-09-989-643-156	Sequence 183, APP
		c	79	23.2	80.0	894	18	US-09-989-643-167	Sequence 184, APP
		c	80	23.2	80.0	894	18	US-09-989-643-169	Sequence 185, APP
		c	81	23.2	80.0	894	18	US-10-753-169-151	Sequence 186, APP
		c	82	23.2	80.0	894	18	US-10-753-169-156	Sequence 187, APP
		c	83	23.2	80.0	894	18	US-10-753-169-161	Sequence 188, APP
		c	84	23.2	80.0	894	18	US-10-753-169-167	Sequence 189, APP
		c	85	23.2	80.0	894	18	US-10-753-169-173	Sequence 190, APP

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	23.2	80.0	29	1.0 US-09-989-643-107 Sequence 107, APP
2	23.2	80.0	28	1.0 US-10-753-169-107 Sequence 107, APP
3	23.2	80.0	70	1.0 US-10-282-122A-1961 Sequence 1961, APP
4	23.2	80.0	70	1.0 US-10-282-122A-2519 Sequence 2519, APP
5	23.2	80.0	70	1.0 US-10-282-122A-2727 Sequence 2727, APP
6	23.2	80.0	111	1.0 US-10-282-122A-2376 Sequence 2376, APP
7	23.2	80.0	130	9.0 US-09-815-242-2973 Sequence 2973, APP
8	23.2	80.0	130	17.0 US-10-282-122A-5535 Sequence 5535, APP
9	23.2	80.0	163	9.0 US-09-815-242-261 Sequence 261, APP
10	23.2	80.0	163	17.0 US-10-282-122A-256 Sequence 256, APP
11	23.2	80.0	17	17.0 US-10-282-122A-2416 Sequence 2416, APP

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OM nucleic - nucleic search, using sw model

Run on: March 16, 2005, 01:07:34 ; Search time 109.865 Seconds
(without alignments)
431.911 Million cell updates/sec

Title: Perfect score: 29

Sequence: 1 aayatgattacnacngngcncaratzga 29

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818130359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *

5: /cgn2_6/ptodata/1/ina/PCRS_COMB.seq: *

6: /cgn2_6/ptodata/1/ina/bactfiles.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description	
1	23.2	80.0	656	3 US-08-936-162A-87 Sequence 87, Appl	
2	23.2	80.0	690	4 US-09-943-682A-2724 Sequence 2724, Appl	
3	23.2	80.0	864	4 US-09-107-433-1775 Sequence 1775, Appl	
4	23.2	80.0	929	4 US-09-710-219-1311 Sequence 1311, Appl	
5	23.2	80.0	1113	4 US-09-889-019A-4624 Sequence 4624, Appl	
6	23.2	80.0	1122	4 US-09-134-000C-1261 Sequence 1261, Appl	
7	23.2	80.0	1122	4 US-09-140-236-22 Sequence 22, Appl	
8	23.2	80.0	1131	4 US-09-107-522A-979 Sequence 979, Appl	
9	23.2	80.0	1155	4 US-09-328-352-1547 Sequence 1547, Appl	
10	23.2	80.0	1185	2 US-08-443-631B-185 Sequence 185, Appl	
11	23.2	80.0	1185	3 US-09-218-197-1 Sequence 1, Appl	
12	23.2	80.0	1185	4 US-09-492-709A-86 Sequence 86, Appl	
13	23.2	80.0	1191	4 US-09-107-533A-1379 Sequence 1379, Appl	
14	23.2	80.0	1191	4 US-09-502-540-8380 Sequence 8380, Appl	
15	23.2	80.0	1197	4 US-09-583-110-747 Sequence 747, Appl	
16	23.2	80.0	1224	4 US-09-232-991A-4775 Sequence 4775, Appl	
C	23.2	80.0	1230	4 US-09-252-911A-4733 Sequence 4733, Appl	
18	23.2	80.0	1230	4 US-09-252-911A-4767 Sequence 4767, Appl	
19	23.2	80.0	1245	3 US-09-134-001C-2540 Sequence 2540, Appl	
C	23.2	80.0	1254	4 US-09-489-029A-3648 Sequence 3648, Appl	
C	21	23.2	80.0	1260	4 US-09-889-03A-3750 Sequence 3750, Appl
C	22	23.2	80.0	1356	4 US-09-252-991A-4740 Sequence 4740, Appl
C	23	23.2	80.0	2377	4 US-09-902-541-3798 Sequence 3798, Appl
C	24	23.2	80.0	2996	3 US-08-961-527-260 Sequence 260, Appl
C	25	23.2	80.0	2997	4 US-09-710-273-3723 Sequence 3723, Appl
C	26	23.2	80.0	3173	4 US-09-581-822-7 Sequence 7, Appl
C	27	23.2	80.0	7035	4 US-09-902-540-878 Sequence 878, Appl
100	15.8	80.0	7035	4 US-09-949-016-126433 Sequence 126433, Appl	

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OM nucleic - nucleic search, using sw model
Run on: March 15, 2005, 22:27:13 ; Search time 2915.62 Seconds
(without alignments)
378.604 Million cell updates/sec

Title: US-10-089-177-664
Perfect score: 29

Sequence: 1 aaayatgatnacnngngcncaratgga 29

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext: 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 500 summaries

Database : EST:*

1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:
10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	23.2	80.0	114	6	CB261354	CB261364 02-E89570-
2	23.2	80.0	4	114	BT360467	BT360467 38736 MA
3	23.2	-80.0	160	4	BG834781	BG834781 353120 MA
4	23.2	80.0	160	4	BGB95149	BG895149 358356 MA
5	23.2	80.0	162	4	BT53234	BT53234 396910 MA
6	23.2	80.0	174	1	AV414173	AV414173 AV414173
7	23.2	80.0	175	4	BTJ162805	BTJ162805 BTJ162805
8	23.2	80.0	194	8	CC059143	CC059143 iii1996.D
9	23.2	80.0	219	2	AW063192	AW063192 TN0356 KR
10	23.2	80.0	220	9	CL898923	CL898923 abg5f11.
11	23.2	80.0	233	7	CF664038	CF664038 K16-B02_P
12	23.2	80.0	266	1	AV418215	AV418215 AV418215
13	23.2	80.0	276	2	AW694494	AW694494 NF07705S
14	23.2	80.0	313	7	CN929943	CN929943 000321AFB
15	23.2	80.0	328	9	CL898925	CL898925 abg5f12.
16	23.2	80.0	344	2	AW063346	AW063346 TN0719 KR
17	23.2	80.0	347	7	CF85624	CF85624 p8ZG01XG
18	23.2	80.0	350	7	T43567	T43567 6830 Lambda
19	23.2	80.0	352	7	CYV513029	CYV513029 TQE7ZT8
c	20	23.2	354	7	CR476349	CR476349 CR7634
c	21	23.2	355	1	A1486103	A1486103 EST244424
22	23.2	80.0	355	7	CN93021	CN93021 000428RF
23	23.2	80.0	380	8	AZ050022	AZ050022 GSSTC09
24	23.2	80.0	385	2	AW064077	AW064077 SP0193 KR
25	23.2	80.0	397	1	AV51304	AV51304 AV51304
26	23.2	80.0	399	6	CB655390	CB655390 OSJNEC8M
27	23.2	80.0	400	7	T04276	T04276 3.23 Lamoda-
28	23.2	80.0	402	1	AV518885	AV518885 AV518885
29	23.2	80.0	402	2	BB521145	BB521145 M17T34JTM
30	23.2	80.0	418	1	AU289247	AU289247 AU289247
31	23.2	80.0	418	4	BG263014	BG263014 WHE0939_G
32	23.2	80.0	422	8	BH749389	BH749389 SALK-0376
33	23.2	80.0	424	5	BO622655	BO622655 CC Contig
34	23.2	80.0	428	4	BM402698	BM402698 SLR0701
35	23.2	80.0	431	1	AV408359	AV408359 AV408359
36	23.2	80.0	435	6	AW040690	AW040690 EST28554
37	23.2	80.0	443	5	BU93125	BU93125 HD12_K10
38	23.2	80.0	446	1	AV422863	AV422863
39	23.2	80.0	449	3	BB354313	BB354313 EST249615
40	23.2	80.0	450	8	CL903203	CL903203 ACAB272A
41	23.2	80.0	451	2	AV940013	AV940013 AV940013
42	23.2	80.0	455	6	CA516269	CA516269 KS095F1
43	23.2	80.0	456	7	M89271	M89271 CEL00D1 Chr
44	23.2	80.0	456	8	BZ349218	BZ349218 hq888e04_g
45	23.2	80.0	466	5	AI4374	AI4374 EST249615
46	23.2	80.0	466	9	CL903203	CL903203 ACAB272A
47	23.2	80.0	467	1	AV940013	AV940013 AV940013
48	23.2	80.0	467	6	CD27518	CD27518 CD27518
49	23.2	80.0	467	7	CO052070	CO052070 McFW20561
50	23.2	80.0	470	9	CL903282	CL903282 ACAB272/A
51	23.2	80.0	471	1	AV422454	AV422454 AV422454
52	23.2	80.0	474	8	BT240239	BT240239 OCAB267M
53	23.2	80.0	475	7	CN942360	CN942360 0109205VB
54	23.2	80.0	475	8	BZ402631	BZ402631 OCAB23TC
55	23.2	80.0	475	4	BT704013	BT704013 RT6506_Y
56	23.2	80.0	479	4	BI267993	BI267993 NF116D041
57	23.2	80.0	480	7	CV042450	CV042450 ta156D07.
58	23.2	80.0	481	8	AZ049142	AZ049142 GSSBR054
59	23.2	80.0	482	1	A1778328	A1778328 EST25207
60	23.2	80.0	482	4	BF639445	BF639445 NE01208I
61	23.2	80.0	485	1	AU060781	AU060781 AU060781
62	23.2	80.0	488	6	CD275520	CD275520 TI43B0155
63	23.2	80.0	490	5	BP070882	BP070882 KB85906_Y
64	23.2	80.0	491	1	AU197422	AU197422 AU197422
65	23.2	80.0	492	5	CD658495	CD658495 ECTESTF34
66	23.2	80.0	493	7	CN547132	CN547132 EST15121
67	23.2	80.0	495	2	BE459790	BE459790 EST144082
68	23.2	80.0	496	5	CD275520	CD275520 TI43B0155
69	23.2	80.0	497	6	CL898925	CL898925 abg5f11.
70	23.2	80.0	498	7	CD606338	CD606338 GENMAD1_0
71	23.2	80.0	501	7	CO746459	CO746459 tahr90f12.
72	23.2	80.0	502	4	BJ803292	BJ803292 BJ803292
73	23.2	80.0	505	7	CK994978	CK994978 041C041.
74	23.2	80.0	505	7	CB331112	CB331112 3529_1_33
75	23.2	80.0	508	6	BE921734	BE921734 EST425503
76	23.2	80.0	510	5	BG445515	BG445515 RHTZ22_45
77	23.2	80.0	510	4	AW675933	AW675933 EST19937
78	23.2	80.0	511	2	BM327118	BM327118 PTC1_22_B
79	23.2	80.0	512	4	BJ758011	BJ758011 BJ758011
80	23.2	80.0	514	4	AV940645	AV940645 AV940645
81	23.2	80.0	515	1	CA524936	CA524936 K12A045B1
82	23.2	80.0	515	6	CD275529	CD275529 TI43B0063
83	23.2	80.0	516	6	AG67461	AG67461 Cyanidios
84	23.2	80.0	516	9	BQ791087	BQ791087 E39701 Chi
85	23.2	80.0	517	5	AL813000	AL813000 AL813000
86	23.2	80.0	518	1	AV442731	AV442731 AV442731
87	23.2	80.0	518	1	AV917158	AV917158 AV917158
88	23.2	80.0	518	2	AW257991	AW257991 68705D08
89	23.2	80.0	518	2	BE44327	BE44327 WHE153_D
90	23.2	80.0	518	9	AL431727	AL431727 T_Gamid
91	23.2	80.0	519	5	BP039049	BP039049 BP039049
92	23.2	80.0	519	6	CA905353	CA905353 PSC66701
93	23.2	80.0	520	1	AV917158	AV917158 AV917158
94	23.2	80.0	521	4	BM066124	BM066124 RS07011A0
95	23.2	80.0	525	4	BG914292	BG914292 Tair1131A
96	23.2	80.0	526	8	AZ30919	AZ30919 GSSBR186
97	23.2	80.0	527	6	CB331196	CB331196 3529_1_34

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OM nucleic - nucleic search, using sw model

Run on:

March 15, 2005, 15:46:58 ; Search time 373.654 Seconds

(Without alignments)

459.443 Million cell updates/sec

Title: US-10-089-177-664

Perfect score: 29

Sequence: 1 aayatgattacnacngngcncaratgga 29

Scoring table: IDENTITY NUC

Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 38780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : N_Geneseq_16Dec04:*

1: geneseq1980s:*
 2: geneseq1990s:*
 3: geneseq2000s:*
 4: geneseq2001as:*
 5: geneseq2001bs:*
 6: geneseq2002as:*
 7: geneseq2002bs:*
 8: geneseq2003as:*
 9: geneseq2003bs:*
 10: geneseq2003cb:*
 11: geneseq2003cb:*
 12: geneseq2004as:*
 13: geneseq2004bs:*

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB	ID	Description
1	23.2	80.0	29	2	AAYV37106		Aav37106 Oligonucleotide
2	23.2	80.0	29	4	AHH00673		Aah00673 Universal
3	23.2	80.0	29	9	ACF05433		Actf05433 Universal
4	23.2	80.0	70	8	ACA1649		Aca1649 Prokaryot
5	23.2	80.0	70	8	ACA14091		Aca14091 Prokaryot
6	23.2	80.0	70	8	ACA14857		Aca14857 Prokaryot
7	23.2	80.0	111	8	ACA14506		Aca14506 Prokaryot
8	23.2	80.0	130	4	AAS50396		Aas50396 Staphyloc
9	23.2	80.0	130	8	ACA17665		Aca17665 Prokaryot
10	23.2	80.0	163	4	AAS47684		Aas47684 Enterococ
11	23.2	80.0	163	8	ACA12386		Aca12386 Prokaryot
12	23.2	80.0	183	8	ACA14546		Aca14546 Prokaryot
13	23.2	80.0	184	4	AAS4608		Aas4608 Staphyloc
14	23.2	80.0	184	8	ACA16888		Aca16888 Prokaryot
15	23.2	80.0	185	6	ACA14269		Aca14269 Prokaryot
16	23.2	80.0	185	8	ACA13996		Aca13996 Prokaryot
17	23.2	80.0	187	4	AAS47621		Aas47621 Enterococ
18	23.2	80.0	187	4	AAS47617		Aas47617 Enterococ
19	23.2	80.0	187	8	ACA12332		Aca12332 Prokaryot
20	23.2	80.0	187	8	ACA12314		Aca12314 Prokaryot
21	23.2	80.0	193	8			Aca1683 Prokaryot
22	23.2	80.0	196	8			Aca15526 Prokaryot
23	23.2	80.0	202	4			Aas47599 Entero
24	23.2	80.0	202	8			Aca1294 Prokaryot
25	23.2	80.0	222	8			Aca13907 Prokaryot
26	23.2	80.0	222	8			Aca14700 Prokaryot
27	23.2	80.0	236	4			Aas47724 Entero
28	23.2	80.0	236	8			Aca12410 Prokaryot
29	23.2	80.0	269	4			Aas47665 Entero
30	23.2	80.0	269	8			Aca12359 Prokaryot
31	23.2	80.0	341	8			Aca14835 Prokaryot
32	23.2	80.0	341	8			Aca13919 Prokaryot
33	23.2	80.0	343	8			Aca14382 Prokaryot
34	23.2	80.0	369	8			Aca14382 Prokaryot
35	23.2	80.0	379	8			Aca14276 Prokaryot
36	23.2	80.0	390	8			Aca14276 Prokaryot
37	23.2	80.0	467	9			Aca14082 Prokaryot
38	23.2	80.0	515	9			Aca14657 Prokaryot
39	23.2	80.0	532	9			Aca14603 Prokaryot
40	23.2	80.0	566	8			Aca131341 Prokaryot
41	23.2	80.0	572	10			Ad229534 Mouse cae
42	23.2	80.0	580	4			Aba8205 Enterococ
43	23.2	80.0	580	9			Aca14877 Prokaryot
44	23.2	80.0	606	9			Acl15425 DNA clone
45	23.2	80.0	608	9			Acl15433 DNA clone
46	23.2	80.0	617	13			Aca131341 Prokaryot
47	23.2	80.0	628	8			Ad229534 Mouse cae
48	23.2	80.0	652	6			Abx66890 Helicobac
49	23.2	80.0	656	2			Aat33947 DNA encod
50	23.2	80.0	657	10			Aar33387 DNA encod
51	23.2	80.0	667	10			Ab241637 N. gonorr
52	23.2	80.0	679	10			Ab241137 N. gonorr
53	23.2	80.0	680	10			Abx66333 Helicobac
54	23.2	80.0	690	10			Ad1024339 Bacteri
55	23.2	80.0	705	8			Aca28337 Prokaryot
56	23.2	80.0	720	10			Ab241639 N. gonorr
57	23.2	80.0	720	10			Ab241141 N. gonorr
58	23.2	80.0	744	5			Aas81943 DNA encod
59	23.2	80.0	779	10			Adff6684 Photorhab
60	23.2	80.0	846	8			Aca3356 Prokaryot
61	23.2	80.0	864	13			Ad193140 Novel S.
62	23.2	80.0	870	10			Aar37149 DNA Sequ
63	23.2	80.0	870	10			Aar37144 Borrelia
64	23.2	80.0	874	5			Aas1943 DNA encod
65	23.2	80.0	879	10			Adff6684 Photorhab
66	23.2	80.0	879	10			Aca3356 Prokaryot
67	23.2	80.0	884	13			Ad193140 Novel S.
68	23.2	80.0	888	4			Aar37149 DNA Sequ
69	23.2	80.0	888	4			Aar37144 Borrelia
70	23.2	80.0	891	2			Aar37160 DNA sequ
71	23.2	80.0	891	2			Aar37152 DNA sequ
72	23.2	80.0	891	2			Aar37153 DNA sequ
73	23.2	80.0	891	2			Aar37154 DNA sequ
74	23.2	80.0	891	2			Aar37155 DNA sequ
75	23.2	80.0	891	2			Aar37156 DNA sequ
76	23.2	80.0	891	2			Aar37157 DNA sequ
77	23.2	80.0	891	2			Aar37158 DNA sequ
78	23.2	80.0	891	2			Aar37159 DNA Sequ
79	23.2	80.0	891	2			Aar37162 DNA sequ
80	23.2	80.0	891	2			Aar01750 Micrococcc
81	23.2	80.0	891	4			Aar01754 Rickettsi
82	23.2	80.0	891	4			Aar01752 Mycoplasm
83	23.2	80.0	891	4			Aar01753 Escherich
84	23.2	80.0	891	4			Aar01753 Neisseria
85	23.2	80.0	891	4			Aar01751 Mycobacte
86	23.2	80.0	891	4			Aar01699 Haemophil
87	23.2	80.0	891	4			Aar01755 Salmonell
88	23.2	80.0	891	4			Aar01760 Ureaplasma
89	23.2	80.0	894	2			Aar37155 DNA sequ
90	23.2	80.0	894	2			Aar37150 DNA Sequ
91	23.2	80.0	894	2			Aar37168 DNA sequ
92	23.2	80.0	894	2			Aar37166 DNA sequ
93	23.2	80.0	894	2			Aar01759 Treponema

OM nucleic - nucleic search, using sw model
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GanCore version 5.1.6

Run on: March 15, 2005, 22:08:52 ; Search time 1102.56 Seconds
Title: US-10-089-177-664 ; (without alignments)
Scoring table: IDENTITY_NUC ; Gapext 1.0
Sequence: 1 aayatgatnacnacngngcngncnacaratgga 29
Searched: 4708233 seqs, 2422707955 residues
Total number of hits satisfying chosen parameters: 9416466
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0% ; Maximum Match 100%
Listing first 500 summaries

Database : GenEmbl:
1: gb_bai:
2: gb_hhg:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vl:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	ID	Description
1	23.2	80.0	29	6 AX109931	AX109931 Sequence
2	23.2	80.0	29	6 BD023039	BD023039 Species-s
3	23.2	80.0	385	6 BD137176	BD137176 Autonomou
4	23.2	80.0	652	6 AK790513	AK790513 Sequence
5	23.2	80.0	654	1 AB025429	AB025429 Streptococ
6	23.2	80.0	654	1 AB025430	AB025430 Streptococ
7	23.2	80.0	656	6 AR194538	AR194538 Sequence
8	23.2	80.0	662	6 AX789399	AX789399 Sequence
9	23.2	80.0	688	1 GU09433	GU09433 Gloeobacter
10	23.2	80.0	690	6 AR377718	AR377718 Sequence
11	23.2	80.0	700	1 AY661424	AY661424 Candidatu
12	23.2	80.0	700	1 AY685053	AY685053 Candidatu
13	23.2	80.0	703	1 AY09445	AY09445 Prochloroth
14	23.2	80.0	703	8 PRM09442	PRM09442 Pandorina m
15	23.2	80.0	705	8 PRM0424	PRM0424 Bryopsis pl
16	23.2	80.0	705	8 CCU094429	CCU094429 Cosmaria co
17	23.2	80.0	705	8 CSU09426	CSU09426 Chlorella ma
18	23.2	80.0	705	8 DMU09431	DMU09431 Desribesia ma
19	23.2	80.0	705	8 SNU09447	SNU09447 Smithora na

20	21	23.2	80.0	705	1	GSU09434
21	22	23.2	80.0	706	8	DPU09432
22	23	23.2	80.0	706	8	GLU09436
23	24	23.2	80.0	706	8	GPU09435
24	25	23.2	80.0	706	8	LSU09437
25	26	23.2	80.0	706	8	MSU09438
26	27	23.2	80.0	706	8	ODU09440
27	28	23.2	80.0	706	8	PSU09441
28	29	23.2	80.0	706	8	VBU09448
29	30	23.2	80.0	706	8	NSU09439
30	31	23.2	80.0	706	8	TSU09440
31	32	23.2	80.0	706	8	UBU09441
32	33	23.2	80.0	732	1	AP217549
33	34	23.2	80.0	732	1	AP217550
34	35	23.2	80.0	732	1	AP217551
35	36	23.2	80.0	732	1	AP217552
36	37	23.2	80.0	732	1	AP217553
37	38	23.2	80.0	747	8	CBR54121
38	39	23.2	80.0	747	8	CLE54122
39	40	23.2	80.0	747	8	CPE54123
40	41	23.2	80.0	747	8	CQF54124
41	42	23.2	80.0	747	8	HCA54125
42	43	23.2	80.0	747	8	HYH54126
43	44	23.2	80.0	747	8	PAE54127
44	45	23.2	80.0	747	8	PDE54128
45	46	23.2	80.0	747	8	UFQ54129
46	47	23.2	80.0	747	8	UFO54130
47	48	23.2	80.0	768	1	AY30355
48	49	23.2	80.0	798	1	AY303555
49	50	23.2	80.0	802	1	AB095671
50	51	23.2	80.0	802	1	AB095672
51	52	23.2	80.0	802	1	AB095669
52	53	23.2	80.0	802	1	AB095668
53	54	23.2	80.0	802	1	AB095667
54	55	23.2	80.0	802	1	AB095670
55	56	23.2	80.0	802	1	AB095673
56	57	23.2	80.0	802	1	AB095674
57	58	23.2	80.0	802	1	AB095675
58	59	23.2	80.0	804	1	AY303556
59	60	23.2	80.0	804	1	AY303571
60	61	23.2	80.0	804	1	PSY18215
61	62	23.2	80.0	812	1	EPG5542
62	63	23.2	80.0	858	8	AY391373
63	64	23.2	80.0	862	1	AY303554
64	65	23.2	80.0	862	1	AY303554
65	66	23.2	80.0	867	8	AY454403
66	67	23.2	80.0	870	8	AY668054
67	68	23.2	80.0	875	8	AY668054
68	69	23.2	80.0	879	8	AY544409
69	70	23.2	80.0	880	8	AY544418
70	71	23.2	80.0	881	8	AY544418
71	72	23.2	80.0	882	8	AY454415
72	73	23.2	80.0	882	8	AY544415
73	74	23.2	80.0	883	8	AY544417
74	75	23.2	80.0	884	8	AY544422
75	76	23.2	80.0	885	8	AY544416
76	77	23.2	80.0	886	8	AY544424
77	78	23.2	80.0	888	6	AX11004
78	79	23.2	80.0	888	6	DO23082
79	80	23.2	80.0	891	6	DO23082
80	81	23.2	80.0	891	6	AX11004
81	82	23.2	80.0	891	6	AX11004
82	83	23.2	80.0	891	6	AX11004
83	84	23.2	80.0	891	6	AX11002
84	85	23.2	80.0	891	6	AX11003
85	86	23.2	80.0	891	6	AX11014
86	87	23.2	80.0	891	6	AX11015
87	88	23.2	80.0	891	6	AX11010
88	89	23.2	80.0	891	6	BD23085
89	90	23.2	80.0	891	6	DO23086
90	91	23.2	80.0	891	6	DO23089
91	92	23.2	80.0	891	6	DO23091